

## SEQUENCE LISTING

## (1) GENERAL INFORMATION:

- (i) APPLICANT: Ceriani, Roberto L.  
Peterson, Jerry A.  
Larocca, David J.
- (ii) TITLE OF THE INVENTION: FUSION PROTEIN WITH 46 KDALTON  
HMFG DIFFERENTIATION ANTIGEN  
BINDING SPECIFICITY, COMPOSITION,  
KIT & METHODS
- (iii) NUMBER OF SEQUENCES: 5
- (iv) CORRESPONDENCE ADDRESS:  
(A) ADDRESSEE: Ratner & Prestia  
(B) STREET: Suite 301  
One Westlakes, Berwyn  
(C) CITY: Valley Forge  
(D) STATE: Pennsylvania  
(E) COUNTRY: USA  
(F) ZIP: 19482
- (v) COMPUTER READABLE FORM:  
(A) MEDIUM TYPE: Floppy disk 3.5"  
(B) COMPUTER: IBM PC compatible  
(C) OPERATING SYSTEM: PC-DOS/MS-DOS 5.0  
(D) SOFTWARE: PatentIn #1.0,  
Version #1.25
- (vi) CURRENT APPLICATION DATA:  
(A) APPLICATION NUMBER:  
(B) FILING DATE: January 2, 2002  
(C) CLASSIFICATION:
- PARENT APPLICATION DATA:  
(A) APPLICATION NUMBER: 08/482,596  
(B) FILING DATE: June 7, 1995  
(C) CLASSIFICATION:
- grand parent APPLICATION DATA:  
(A) APPLICATION NUMBER: 07/607,538  
(B) FILING DATE:  
(C) CLASSIFICATION:
- (viii) ATTORNEY/AGENT INFORMATION:  
(A) NAME: Amzel, Viviana  
(B) REGISTRATION No.: 30,930  
(C) REFERENCE/DOCKET No: CRFC-047
- (ix) TELECOMMUNICATION INFORMATION:  
(A) TELEPHONE: (610) 407-0700

(B) TELEFAX: (610) 407-0701  
(C) TELEX: N.A.

(2) INFORMATION FOR SEQ ID NO:1:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 1384 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: both  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1:

GATTTTCATCC	ATGATGTTAA	TAAAAACAC	AAGGAGTTTG	TGGGTAAC TG	50
GAACAAAAAC	GCGGTGCATG	TCAACCTGTT	TGAGACCCCT	GTGGAGGCTC	100
AGTACGTGAG	ATTGTACCCC	ACGAGCTGCC	ACACGGCCTG	CACTCTGCGC	150
TTTGAGCTAC	TGGGCTGTGA	GCTGAACGGA	TGCGCCAATC	CCCTGGGCCT	200
GAAGAATAAC	AGCATCCCTG	ACAAGCAGAT	CACGGCCTCC	AGCAGCTACA	250
AGACCTGGGG	CTTGCACTCT	TTCAGCTGGA	ACCCCTCCTA	TGCACGGCTG	300
GACAAGCAGG	GCAACTTCAA	CGCCTGGGTT	GCGGGGAGCT	ACGGTAACGA	350
TCAGTGGCTG	CAGGTGGACC	TGGGCTCCTC	GAAGGAGGTG	ACAGGCATCA	400
TCACCCAGGG	GGCCCGTAAC	TTTGGCTCTG	TCCAGTTTGT	GGCATCCTAC	450
AAGGTTGCCT	ACAGTAATGA	CAGTGCGAAC	TGGACTGAGT	ACCAGGACCC	500
CAGGACTGGC	AGCAGTAAGA	TCTTCCCTGG	CAACTGGGAC	AACCACTCCC	550
ACAAGAAGAA	CTTGTTTGAG	ACGCCCATCC	TGGCTCGCTA	TGTGCGCATC	600
CTGCCTGTAG	CCTGGCACAA	CCGCACTGCC	CTGCGCCTGG	AGCTGCTGGG	650
CTGTTAGTGG	CCACCTGCCA	CCCCAGGTC	TTCCTGCTTT	CCATGGGCCC	700
GCTGCCTCTT	GGCTTCTCAG	CCCCTTTAAA	TCACCATAGG	GCTGGGGACT	750
GGGGAAGGGG	AGGGTGTTCA	GAGGCAGCAC	CACCACACAG	TCACCCCTCC	800
CTCCCTCTTT	CCCACCCTCC	ACCTCTCACG	GGCCCTGCCC	CAGCCCCTAA	850
GCCCCGTCCC	CTAACCCCCA	GTCCCTCACTG	TCCTGTTTTT	TTAGGCACTG	900
AGGGATCTGA	GTAGGTCTGG	GATGGACAGG	AAAGGGCAAA	GTAGGGCGTG	950
TGGTTTCCCT	GCCCCCTGTCC	GGACCGCCGA	TCCCAGGTGC	GTGTGTCTCT	1000
GTCTCTCCTA	GCCCCCTCTCT	CACACATCAC	ATTCCCATGG	TGGCCTCAAG	1050
AAAGGCCCGG	AAGCCCCAGG	CTGGAGATAA	CAGCCTCTTG	CCCGTCGGCC	1100
CTGCGTCGGC	CCTGGGGTAC	CATGTGCCAC	AACTGCTGTG	GCCCCCTGTC	1150
CCCAAGACAC	TTCCCTTGT	CTCCCTGGTT	GCCTCTCTTG	CCCCTTGTCC	1200
TGAAGCCCAG	CGACACAGAA	GGGGGTGGGG	CGGGTCTATG	GGGAGAAAGG	1250
GAGCGAGGTC	AGAGGAGGGC	ATGGGTGGGC	AGGGTGGGCG	TTTGGGGCCC	1300
TCATGCTGGC	TTTTCACCCC	AGAGGACACA	GGCAGCTTCC	AAAATATATT	1350
TATCTTCTTC	ACGGGAAAAA	AAAAAAAAAA	ACCG		1384

(2) INFORMATION FOR SEQ ID NO:2:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 218 amino acids  
(B) TYPE: amino acid  
(C) STRANDEDNESS:  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(v) FRAGMENT TYPE:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2:

```

Asp Phe Ile His Asp Val Asn Lys Lys His Lys Glu Phe Val
 1      5      10
Gly Asn Trp Asn Lys Asn Ala Val His Val Asn Leu Phe Glu
15      20      25
Thr Pro Val Glu Ala Gln Tyr Val Arg Leu Tyr Pro Thr Ser
30      35      40
Cys His Thr Ala Cys Thr Leu Arg Phe Glu Leu Leu Gly Cys
45      50      55
Glu Leu Asn Gly Cys Ala Asn Pro Leu Gly Leu Lys Asn Asn
60      65      70
Ser Ile Pro Asp Lys Gln Ile Thr Ala Ser Ser Ser Tyr Lys
75      80
Thr Trp Gly Leu His Leu Phe Ser Trp Asn Pro Ser Tyr Ala
85      90      95
Arg Leu Asp Lys Gln Gly Asn Phe Asn Ala Trp Val Ala Gly
100      105      110
Ser Tyr Gly Asn Asp Gln Trp Leu Gln Val Asp Leu Gly Ser
115      120      125
Ser Lys Glu Val Thr Gly Ile Ile Thr Gln Gly Ala Arg Asn
130      135      140
Phe Gly Ser Val Gln Phe Val Ala Ser Tyr Lys Val Ala Tyr
145      150
Ser Asn Asp Ser Ala Asn Trp Thr Glu Tyr Gln Asp Pro Arg
155      160      165
Thr Gly Ser Ser Lys Ile Phe Pro Gly Asn Trp Asp Asn His
170      175      180
Ser His Lys Lys Asn Leu Phe Glu Thr Pro Ile Leu Ala Arg
185      190      195
Tyr Val Arg Ile Leu Pro Val Ala Trp His Asn Arg Ile Ala
200      205      210
Leu Arg Leu Glu Leu Leu Gly Cys
215

```

## (2) INFORMATION FOR SEQ ID NO:3:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 217  
 (B) TYPE: amino acid  
 (C) STRANDEDNESS:  
 (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: protein

## (v) FRAGMENT TYPE:

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:3:

```

Phe Ile His Asp Val Asn Lys Lys His Lys Glu Phe Val Gly
 1      5      10
Asn Trp Asn Lys Asn Ala Val His Val Asn Leu Phe Glu Thr
15      20      25
Pro Val Glu Ala Gln Tyr Val Arg Leu Tyr Pro Thr Ser Cys
30      35      40
His Thr Ala Cys Thr Leu Arg Phe Glu Leu Leu Gly Cys Glu
45      50      55
Leu Asn Gly Cys Ala Asn Pro Leu Gly Leu Lys Asn Asn Ser
60      65      70
Ile Pro Asp Lys Gln Ile Thr Ala Ser Ser Ser Tyr Lys Thr
75      80
Trp Gly Leu His Leu Phe Ser Trp Asn Pro Ser Tyr Ala Arg
85      90      95
Leu Asp Lys Gln Gly Asn Phe Asn Ala Trp Val Ala Gly Ser

```

```

      100                      105                      110
Tyr Gly Asn Asp Gln Trp Leu Gln Val Asp Leu Gly Ser Ser
      115                      120                      120
Lys Glu Val Thr Gly Ile Ile Thr Gln Gly Ala Arg Asn Phe
      130                      135                      140
Gly Ser Val Gln Phe Val Ala Ser Tyr Lys Val Ala Tyr Ser
      145                      150
Asn Asp Ser Ala Asn Trp Thr Glu Tyr Gln Asp Pro Arg Thr
155                      160                      165
Gly Ser Ser Lys Ile Phe Pro Gly Asn Trp Asp Asn His Ser
      170                      175                      180
His Lys Lys Asn Leu Phe Glu Thr Pro Ile Leu Ala Arg Tyr
      185                      190                      195
Val Arg Ile Leu Pro Val Ala Trp His Asn Arg Ile Ala Leu
      200                      205                      210
Arg Leu Glu Leu Leu Gly Cys
      215                      217

```

## (2) INFORMATION FOR SEQ ID NO:4:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 218 amino acids
  - (B) TYPE: amino acid
  - (C) STRANDEDNESS:
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(v) FRAGMENT TYPE:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:4:

```

Phe Lys Gly Asn Ser Thr Arg Asn Val Met Tyr Phe Asn Gly
 1      5      10
Asn Ser Asp Ala Ser Thr Ile Lys Glu Asn Gln Phe Asp Pro
15      20      25
Pro Ile Val Ala Arg Tyr Ile Arg Ile Ser Pro Thr Arg Ala
30      35      40
Tyr Asn Arg Pro Thr Leu Arg Leu Glu Leu Gln Gly Cys Glu
45      50      55
Val Asn Gly Cys Ser Thr Pro Leu Gly Met Glu Asn Gly Lys
60      65      70
Ile Glu Asn Lys Gln Ile Thr Ala Ser Ser Phe Lys Lys Ser
75      80
Trp Trp Gly Asp Tyr Trp Glu Pro Phe Arg Ala Arg Leu Asn
85      90      95
Ala Gln Gly Arg Val Asn Ala Trp Gln Ala Lys Ala Asn Asn
100      105      110
Asn Lys Gln Trp Leu Glu Ile Asp Leu Leu Lys Ile Lys Lys
115      120      125
Ile Thr Ala Ile Ile Thr Gln Gly Cys Lys Ser Leu Ser Ser
130      135      140
Glu Met Tyr Val Lys Ser Tyr Thr Ile His Tyr Ser Glu Gln
145      150
Gly Val Glu Trp Lys Pro Tyr Arg Leu Lys Ser Ser Met Val
155      160      165
Asp Lys Ile Phe Glu Gly Asn Thr Asn Thr Lys Gly His Val
170      175      180
Lys Asn Phe Phe Asn Pro Pro Ile Ile Ser Arg Phe Ile Arg
185      190      195
Val Ile Pro Lys Thr Trp Asn Gln Ser Ile Ala Leu Arg Leu
200      205      210

```

Glu Leu Phe Gly Cys Asp Ile Tyr  
                   215                  218

(2) INFORMATION FOR SEQ ID NO:5:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 218  
 (B) TYPE: amino acid  
 (C) STRANDEDNESS:  
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(v) FRAGMENT TYPE:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:5:

Tyr	Arg	Gly	Asn	Ser	Thr	Gly	Thr	Leu	Met	Val	Phe	Phe	Gly
1				5					10				
Asn	Val	Asp	Ser	Ser	Gly	Ile	Lys	His	Asn	Ile	Phe	Asn	Pro
15					20					25			
Pro	Ile	Ile	Ala	Arg	Tyr	Ile	Arg	Leu	His	Pro	Thr	His	Tyr
	30					35					40		
Ser	Ile	Arg	Ser	Thr	Leu	Arg	Met	Glu	Leu	Met	Gly	Cys	Asp
		45					50					55	
Leu	Asn	Ser	Cys	Ser	Met	Pro	Leu	Gly	Met	Glu	Ser	Lys	Ala
			60					65					70
Ile	Ser	Asp	Ala	Gln	Ile	Thr	Ala	Ser	Ser	Tyr	Phe	Thr	Asn
				75					80				
Met	Phe	Ala	Thr	Trp	Ser	Pro	Ser	Lys	Ala	Arg	Leu	His	Leu
	85				90					95			
Gln	Gly	Arg	Ser	Asn	Ala	Trp	Arg	Pro	Gln	Val	Asn	Asn	Pro
	100					105					110		
Lys	Glu	Trp	Leu	Gln	Val	Asp	Phe	Gln	Lys	Thr	Met	Lys	Val
		115					120					125	
Thr	Gly	Val	Thr	Thr	Gln	Gly	Val	Lys	Ser	Leu	Leu	Thr	Glu
			130					135					140
Met	Tyr	Val	Lys	Glu	Phe	Leu	Ile	Ser	Ser	Ser	Gln	Asp	Gly
				145					150				
His	Gln	Trp	Thr	Leu	Phe	Phe	Gln	Asn	Gly	Lys	Val	Lys	Val
	155				160					165			
Phe	Gln	Gly	Asn	Gln	Asp	Ser	Phe	Thr	Pro	Val	Val	Asn	Ser
	170					175					180		
Leu	Asp	Pro	Pro	Leu	Leu	Thr	Arg	Tyr	Leu	Arg	Ile	His	Pro
		185					190					195	
Gln	Ser	Trp	Val	His	Gln	Ile	Ala	Leu	Arg	Met	Glu	Val	Leu
		200						205					210
Gly	Cys	Glu	Ala	Gln	Asp	Leu	Tyr						
				215			218						